

| UniprotKB ID | Entry name | organism | full name | oglcnacscore | oglcnac sites | phosphorylation sites | PMIDS | sequence | intracellular | extracellular | cytosol | nucleus | mitochondrion | endoplasmic reticulum | golgi apparatus | plasma membrane | extracellular region |
|--------------|------------|-------------------|-----------|--------------|---------------|-----------------------|----------|---|---------------|---------------|---------|---------|---------------|-----------------------|-----------------|-----------------|----------------------|
| D4A628 | D4A628_RAT | Rattus norvegicus | NaN | 23.439218 | NaN | NaN | 38843836 | MSLPRRSGKRRRSSSSGDSFSFGSD GDSCVSPQLLCRPVLSPPPGLGRGR RLAGTGTCKQRVSDDDQIDQLLANW GLPKAVLEKYHNFVGVKMFVQAE CLLLGQVLEKGLVYSAPTSAGKTLV AELLILKRVLETRKKALFILPFVSVAK EKYYLQSLFQEVGKVDGYMGSTS PTGRFSSLDVAVCTIERANGLINRLI EENKMDLLGTVVVDELHMLGDSHR GYLLELLLTVCVTRKSASCQADSA SALACAVQIVGMSATLPNLQLVASW LNAELYHTDFRPVPLESIKVGNSIY DSSMKLVREFQPLLQVKGDEDHIVS LCYETVRDNHNSLVFPCSKKWCCEK ADIIAREFYNLHHQPEGLVKSSEFPP VILDQKSLLEVIDQLKRSPSGLDSVL KNTVPWGVAFHHAGLTFEERDIEG AFRQGLIRVLAATSTLSSGVNLPARR VIIRTPVFGGQPLDILTYQMVGGRAG RKGVDTMGESILVCKNSEKSKGIALL QGSLEPVHSCLQSQGEVSTMIRAIL EIIVSGVASTSQDMQTYAACTFLAAD VKEGKQGIQRNRDDVQRGAVDACV TWLENEFIQAAEPSDGTGGKVYHP THLGSATLSSLSPTDTLDIFADLQR AMKGFVLENDLHIVYLTPVFEDWT SIDWYRFFCLWEKLPTSMKRVAELV GVEEGFLARCVKGVVARTERQHRQ MAIHKRFFTSVLVLDLISEIPLKEINQ KYGCGNRGQIQSLQSSAAVYAGMITV FSNRLGWHNMELLLSQFQKRLTFGI QRELCDLIRVSSLNAQRARFLYASGF LTVADLARADTVEVEAALKDALPFKS ARKAVDEEEAAEERRSMRTIWWAG KSLSAREAAALIVEEAKVILQQDLIE MGVQWGPSPHPLSSSTHSLTSGSEVK EHTFKSQTKSSHKRLASKSRNSMRV SGSNGKQSPGAGQGLDECRRERPSL CKFQGNHEIQTPSVYRARKRTSLGV NKEMLRTSLKEGKPKSTKEVLQTLSE EKTRKAALSFSEQANNSFPSPGRDR KYRKKSWGSSPMSDSVMHRDDLQG QTMCKSTLCEDPQKSLEEONTEYRS PGLFAKNVFCAKEKCNKTSFPLQM QQPCLRRKPESGAAVDHSVAVSQNK NVVEQPPGAPDRRRGLAAHGRAEV NEVLTENGTESQLHDTHPVSQCLE NHSEKQNTCTRQKTLTEGQAGISH VTRGSNDLTPIRCERLKLNSKEHDS NPCPQALGTNAGRTEAPQSSEALGO AGGQCENLLNSPGIQEKSAHATNK TEHSHVANQAFCDGDSLYLDTQSE EIIEMATKNATQGAEAAAGITEEGSA TONEPHSTTGGQHIPGAANTDHVDR KNTESVKENPEKNIDRRTPHSLIFHS PTPQGGNSACFKENEHSVTDSQLNS FLOGLETQDKPIIPLAPQMRTSTGVE EESLPETSLNMSDSLFDSEFGDSFG QRQSLDVKAKQPLLEMTPNHFHN PPYPQEDPVMTPHMSEPQGTLERM ACLSGESIIFSEIDSAQVIEALDNMAA FYMQENCNPITLKTPEPRDLAALGNE CPQGEVVRGEQHEGSSKPKFMEIN QDNSFTWSAASFNLSPELQRILDKV STPRENEPELMHADLSCFEENSTE SHERQDMNSDLGTVQRTSFLPSNG VKSRTGLESKAKHGGASSALPHKA AADDNGLIPPTPLPASASASASKLAL PEILGTSVKHQKASCLFDSFSDNQ QDLSQELRDSLKSDSGSVVDTSFLL QSQDGLLLTQASCSSSLAHDVAVSD QILFQTFVKEWQCQKRFSISLACEK MTSSTSSKTATIGRKLQVNSPQEA | False | False | 2.225 | 3.867 | 1.54 | False | 2.0 | False | False |

SVEDDGFPVHGSDCAVVVGLAVCW
GGKDAYLSLQKEQKQSEMSPSLAP
PPLDATLTVKERMEYLQSCLOKKS
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